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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/961,400

DATE: 08/05/2002
TIME: 14:33:36

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3 <110> APPLICANT: RYBAK, SUSANNA M.
4 GOLDENBERG, DAVID M.
5 NEWTON, DIANNE L.
7 <120> TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
8 CELLS
10 <130> FILE REFERENCE: 018733/1059
12 <140> CURRENT APPLICATION NUMBER: 09/961,400
13 <141> CURRENT FILING DATE: 2001-09-25
15 <150> PRIOR APPLICATION NUMBER: 09/622,613
16 <151> PRIOR FILING DATE: 2000-08-17
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/06641
19 <151> PRIOR FILING DATE: 1999-03-26
21 <150> PRIOR APPLICATION NUMBER: 60/079,751
22 <151> PRIOR FILING DATE: 1998-03-26
24 <160> NUMBER OF SEQ ID NOS: 43
26 <170> SOFTWARE: PatentIn Ver. 2.1
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30 <212> TYPE: DNA
31 <213> ORGANISM: Rana pipiens
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35 <222> LOCATION: (1)..(312)
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40 1 5 10 15
42 gtt gac tgt aat aat atc atg tca aca aac ttg ttc cac tgc aag gac 96
43 Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys Asp
44 20 25 30
46 aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc tgt 144
47 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
48 35 40 45
50 aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt tat 192
51 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Ser Glu Phe Tyr
52 50 55 60
54 ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta aag 240
55 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
56 65 70 75 80
58 aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca gta 288
59 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val
60 85 90 95
62 cat ttc gtg ggt gtc gga cat tgc 312

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76 Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys Asp
77 20 25 30
79 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
80 35 40 45
82 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe Tyr
83 50 55 60
85 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
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88 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val
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103 <222> LOCATION: (1)..(312)
105 <400> SEQUENCE: 3
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107 Gln Asp Trp Leu Thr Phe Gln Lys Lys His Leu Thr Asn Thr Arg Asp
108 1 5 10 15
110 gtt gac tgt aat aat atc ctg tca aca aac ttg ttc cac tgc aag gac 96
111 Val Asp Cys Asn Asn Ile Leu Ser Thr Asn Leu Phe His Cys Lys Asp
112 20 25 30
114 aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc tgt 144
115 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
116 35 40 45
118 aaa gga att ata gcc tcc aaa aat gtg tta act acc ttt gag ttt tat 192
119 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe Tyr
120 50 55 60
122 ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta aag 240
123 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
124 65 70 75 80
126 aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca gta 288
127 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val
128 85 90 95
130 cat ttc gtg ggt gtc gga cat tgc 312
131 His Phe Val Gly Val Gly His Cys

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 144 Val Asp Cys Asn Asn Ile Leu Ser Thr Asn Leu Phe His Cys Lys Asp
 145 20 25 30
 147 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
 148 35 40 45
 150 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe Tyr
 151 50 55 60
 153 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
 154 65 70 75 80
 156 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val
 157 85 90 95
 159 His Phe Val Gly Val Gly His Cys
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 171 <222> LOCATION: (1)..(315)
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 176 1 5 10 15
 178 gat gtt gac tgt aat aat atc atg tca aca aac ttg ttc cac tgc aag 96
 179 Asp Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys
 180 20 25 30
 182 gac aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc 144
 183 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
 184 35 40 45
 186 tgt aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt 192
 187 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
 188 50 55 60
 190 tat ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta 240
 191 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
 192 65 70 75 80
 194 aag aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca 288
 195 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
 196 85 90 95
 198 gta cat ttc gtg ggt gtc gga cat tgc 315
 199 Val His Phe Val Gly Val Gly His Cys
 200 100 105

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205 <212> TYPE: PRT
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208 <400> SEQUENCE: 6
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210 1 5 10 15
212 Asp Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys
213 20 25 30
215 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
216 35 40 45
218 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
219 50 55 60
221 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
222 65 70 75 80
224 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
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227 Val His Phe Val Gly Val Gly His Cys
228 100 105
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234 <212> TYPE: DNA
235 <213> ORGANISM: Rana pipiens
237 <220> FEATURE:
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242 atg caa gac tgg ctt acg ttt cag aag aac cac ctg aca aac acc cgg 48
243 Met Gln Asp Trp Leu Thr Phe Gln Lys Lys His Leu Thr Asn Thr Arg
244 1 5 10 15
246 gat gtt gac tgt aat aat atc ctg tca aca aac ttg ttc cac tgc aag 96
247 Asp Val Asp Cys Asn Asn Ile Leu Ser Thr Asn Leu Phe His Cys Lys
248 20 25 30
250 gac aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc 144
251 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
252 35 40 45
254 tgt aaa gga att ata gcc tcc aaa aat gtg tta act acc ttt gag ttt 192
255 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe
256 50 55 60
258 tat ctc tct gat tgc aat gca aca agc agg cct tgc aag tat aaa tta 240
259 Tyr Leu Ser Asp Cys Asn Ala Thr Ser Arg Pro Cys Lys Tyr Lys Leu
260 65 70 75 80
262 aag aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca 288
263 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
264 85 90 95
266 gta cat ttc gtg ggt gtc gga cat tgc 315
267 Val His Phe Val Gly Val Gly His Cys
268 100 105
271 <210> SEQ ID NO: 8

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 281 20 25 30
 283 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
 284 35 40 45
 286 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe
 287 50 55 60
 289 Tyr Leu Ser Asp Cys Asn Ala Thr Ser Arg Pro Cys Lys Tyr Lys Leu
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 305 <400> SEQUENCE: 9
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 309 His Leu Thr Asn Thr Arg Asp Val Asp Cys Asn Asn Ile Leu Ser Thr
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 312 Asn Leu Phe His Cys Lys Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro
 313 35 40 45
 315 Glu Pro Val Lys Ala Ile Cys Lys Gly Ile Ile Ala Ser Lys Asn Val
 316 50 55 60
 318 Leu Thr Thr Ser Glu Phe Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg
 319 65 70 75 80
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 339 Ser Asp Trp Leu Thr Phe Gln Lys Lys His Leu Thr Asn Thr Arg Asp
 340 1 5 10 15
 342 gtt gac tgt aat aat atc atg tca aca aac ttg ttc cac tgc aag gac 96

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